

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-30.rni.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 5.02867 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatctggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	100.0	2868	3	US-08-780-562-8
2	23	100.0	3097	2	US-08-599-455B-1
3	23	100.0	3097	3	US-09-069-781B-1
4	23	100.0	3097	3	US-09-137-132-1
5	23	100.0	3097	3	US-08-864-564A-1
6	23	100.0	3097	3	US-09-094-410-1

	7	23	100.0	3097	3	US-08-708-123D-1	Sequence 1, Appli
	8	23	100.0	3097	3	US-08-583-153A-1	Sequence 1, Appli
	9	23	100.0	3097	3	US-08-570-142D-1	Sequence 1, Appli
	10	23	100.0	3097	3	US-08-638-524B-1	Sequence 1, Appli
	11	23	100.0	3097	4	US-09-950-149-1	Sequence 1, Appli
	12	23	100.0	3495	3	US-08-827-962-17	Sequence 17, Appl
	13	23	100.0	3650	3	US-08-837-635-5	Sequence 5, Appli
	14	23	100.0	3650	3	US-08-837-635-7	Sequence 7, Appli
	15	23	100.0	3650	3	US-08-827-962-16	Sequence 16, Appl
	16	23	100.0	3650	3	US-08-803-346-2	Sequence 2, Appli
	17	23	100.0	3854	2	US-08-599-455B-42	Sequence 42, Appl
	18	23	100.0	3854	3	US-09-069-781B-42	Sequence 42, Appl
	19	23	100.0	3854	3	US-09-137-132-42	Sequence 42, Appl
	20	23	100.0	3854	3	US-08-864-564A-42	Sequence 42, Appl
	21	23	100.0	3854	3	US-09-094-410-42	Sequence 42, Appl
	22	23	100.0	3854	3	US-08-708-123D-42	Sequence 42, Appl
	23	23	100.0	3854	3	US-08-638-524B-42	Sequence 42, Appl
	24	23	100.0	3854	4	US-09-950-149-42	Sequence 42, Appl
c	25	19.8	86.1	3018	3	US-09-949-016-4756	Sequence 4756, Ap
c	26	19.8	86.1	52494	3	US-09-949-016-16498	Sequence 16498, A
	27	18.8	81.7	123	3	US-09-313-294A-1350	Sequence 1350, Ap
	28	17.8	77.4	601	3	US-09-949-001-334	Sequence 334, App
	29	17.8	77.4	312957	3	US-09-949-001-31	Sequence 31, Appl
	30	17.8	77.4	312972	3	US-09-949-001-34	Sequence 34, Appl
c	31	17.2	74.8	543	3	US-09-248-796A-7493	Sequence 7493, Ap
	32	17.2	74.8	588	3	US-09-248-796A-3595	Sequence 3595, Ap
	33	17.2	74.8	599	3	US-09-917-254-20	Sequence 20, Appl
	34	17.2	74.8	599	4	US-09-880-107-3826	Sequence 3826, Ap
	35	17.2	74.8	601	3	US-09-949-016-56677	Sequence 56677, A
	36	17.2	74.8	150032	3	US-09-949-016-14321	Sequence 14321, A
	37	17.2	74.8	636591	3	US-09-949-016-11808	Sequence 11808, A
	38	17.2	74.8	636591	3	US-09-949-016-13388	Sequence 13388, A
	39	17.2	74.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	40	17.2	74.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
c	41	16.8	73.0	601	3	US-09-949-002-8614	Sequence 8614, Ap
c	42	16.8	73.0	2088	3	US-09-134-001C-1504	Sequence 1504, Ap
c	43	16.8	73.0	2265	3	US-09-710-279-1295	Sequence 1295, Ap
c	44	16.8	73.0	2982	3	US-09-710-279-4062	Sequence 4062, Ap
c	45	16.8	73.0	3041	3	US-09-710-279-4193	Sequence 4193, Ap

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:48:31 ; Search time 37.8753 Seconds
(without alignments)
7461.730 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatctggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	23	100.0	2679	6	US-10-278-733-14	Sequence 14, Appl
2	23	100.0	2868	2	US-08-779-457-8	Sequence 8, Appli
3	23	100.0	2868	6	US-10-214-802-8	Sequence 8, Appli
4	23	100.0	2868	9	US-10-921-710-8	Sequence 8, Appli
5	23	100.0	2868	15	US-11-192-219-8	Sequence 8, Appli
6	23	100.0	3097	6	US-10-079-625-1	Sequence 1, Appli
7	23	100.0	3097	16	US-11-202-330-1	Sequence 1, Appli
8	23	100.0	3489	6	US-10-278-733-18	Sequence 18, Appl
9	23	100.0	3656	6	US-10-226-579-1	Sequence 1, Appli
10	23	100.0	3799	16	US-11-136-527-2058	Sequence 2058, Ap
11	23	100.0	3854	6	US-10-079-625-42	Sequence 42, Appl
12	23	100.0	3854	16	US-11-202-330-42	Sequence 42, Appl
c 13	19.8	86.1	598	4	US-09-925-065A-659704	Sequence 659704,
c 14	19.8	86.1	598	5	US-09-925-065A-659704	Sequence 659704,
c 15	19.8	86.1	610	4	US-09-925-065A-571055	Sequence 571055,
c 16	19.8	86.1	610	5	US-09-925-065A-571055	Sequence 571055,
c 17	19.8	86.1	616	12	US-10-301-480-292735	Sequence 292735,
c 18	19.8	86.1	616	12	US-10-301-480-906144	Sequence 906144,
19	19.8	86.1	620	4	US-09-925-065A-204616	Sequence 204616,
20	19.8	86.1	620	5	US-09-925-065A-204616	Sequence 204616,
c 21	19.8	86.1	6021	3	US-09-819-247-1	Sequence 1, Appli
c 22	19.8	86.1	6021	8	US-10-428-225-1	Sequence 1, Appli
c 23	19.8	86.1	6021	10	US-10-450-763-14985	Sequence 14985, A
c 24	19.8	86.1	6021	12	US-10-960-414-487	Sequence 487, App
c 25	19.8	86.1	100596	10	US-10-737-082-92	Sequence 92, Appl
c 26	19.8	86.1	100596	10	US-10-765-790-92	Sequence 92, Appl
27	18.8	81.7	1748	8	US-10-424-599-17613	Sequence 17613, A
c 28	18.4	80.0	588	12	US-10-301-480-479059	Sequence 479059,
c 29	18.4	80.0	588	12	US-10-301-480-1092468	Sequence 1092468,
c 30	18.4	80.0	596	4	US-09-925-065A-413011	Sequence 413011,
c 31	18.4	80.0	596	5	US-09-925-065A-413011	Sequence 413011,
32	18.4	80.0	5763	7	US-10-311-455-1262	Sequence 1262, Ap
c 33	18.2	79.1	168	9	US-10-425-115-35044	Sequence 35044, A
34	18.2	79.1	288	9	US-10-425-115-162806	Sequence 162806,
c 35	18.2	79.1	500	4	US-09-925-065A-165765	Sequence 165765,
c 36	18.2	79.1	500	5	US-09-925-065A-165765	Sequence 165765,
c 37	18.2	79.1	508	12	US-10-301-480-258037	Sequence 258037,
c 38	18.2	79.1	508	12	US-10-301-480-871446	Sequence 871446,
39	18.2	79.1	1109	8	US-10-425-114-14290	Sequence 14290, A
40	18.2	79.1	1201	9	US-10-425-115-156297	Sequence 156297,
41	18.2	79.1	3673778	7	US-10-312-841-1	Sequence 1, Appli
c 42	17.8	77.4	433	4	US-09-925-065A-665207	Sequence 665207,
c 43	17.8	77.4	433	5	US-09-925-065A-665207	Sequence 665207,
c 44	17.8	77.4	463	8	US-10-767-701-11953	Sequence 11953, A
c 45	17.8	77.4	565	4	US-09-925-065A-631937	Sequence 631937,

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 3.35245 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatctgtggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	19.8	86.1	6021	7	US-11-266-748A-32165	Sequence 32165, A
c	2	19.8	86.1	6021	7	US-11-266-748A-32166	Sequence 32166, A
c	3	19.8	86.1	6021	7	US-11-266-748A-32167	Sequence 32167, A
c	4	18.8	81.7	1757	6	US-10-953-349-18576	Sequence 18576, A
c	5	18.8	81.7	1788	7	US-11-216-545-5800	Sequence 5800, Ap
c	6	17.8	77.4	1472	6	US-10-953-349-29147	Sequence 29147, A
	7	17.2	74.8	482	7	US-11-266-748A-169065	Sequence 169065, A
	8	17.2	74.8	635	7	US-11-266-748A-54489	Sequence 54489, A

	9	17.2	74.8	640	7	US-11-266-748A-263107	Sequence 263107,
c	10	17.2	74.8	640	7	US-11-266-748A-323624	Sequence 323624,
	11	17.2	74.8	752	7	US-11-266-748A-362030	Sequence 362030,
	12	17.2	74.8	752	7	US-11-266-748A-387811	Sequence 387811,
c	13	17.2	74.8	752	7	US-11-266-748A-445409	Sequence 445409,
	14	17.2	74.8	945	7	US-11-266-748A-188794	Sequence 188794,
	15	17.2	74.8	961	7	US-11-266-748A-397745	Sequence 397745,
c	16	17.2	74.8	961	7	US-11-266-748A-468791	Sequence 468791,
	17	17.2	74.8	1094	7	US-11-266-748A-73574	Sequence 73574, A
c	18	17.2	74.8	1094	7	US-11-266-748A-126385	Sequence 126385,
	19	17.2	74.8	6432	7	US-11-217-529-82021	Sequence 82021, A
	20	17.2	74.8	11429	6	US-10-517-441-479	Sequence 479, App
	21	17.2	74.8	11429	6	US-10-517-441-753	Sequence 753, App
c	22	16.8	73.0	333	7	US-11-266-748A-172240	Sequence 172240,
	23	16.8	73.0	333	7	US-11-266-748A-245535	Sequence 245535,
c	24	16.8	73.0	1147	7	US-11-266-748A-94013	Sequence 94013, A
	25	16.8	73.0	1147	7	US-11-266-748A-146824	Sequence 146824,
c	26	16.8	73.0	1781	6	US-10-953-349-35542	Sequence 35542, A
	27	16.6	72.2	487	7	US-11-266-748A-307010	Sequence 307010,
	28	16.6	72.2	1000	7	US-11-266-748A-220653	Sequence 220653,
	29	16.6	72.2	1000	7	US-11-266-748A-284005	Sequence 284005,
c	30	16.6	72.2	1000	7	US-11-266-748A-335434	Sequence 335434,
	31	16.6	72.2	1000	7	US-11-266-748A-393867	Sequence 393867,
c	32	16.6	72.2	1000	7	US-11-266-748A-464913	Sequence 464913,
c	33	16.6	72.2	1734	7	US-11-217-529-2269	Sequence 2269, Ap
	34	16.6	72.2	2906	7	US-11-266-748A-24954	Sequence 24954, A
	35	16.6	72.2	3088	6	US-10-449-902-20524	Sequence 20524, A
c	36	16.4	71.3	1050	6	US-10-471-571A-2467	Sequence 2467, Ap
	37	16.4	71.3	1322	7	US-11-216-545-1586	Sequence 1586, Ap
	38	16.4	71.3	1954	7	US-11-140-450-110	Sequence 110, App
	39	16.4	71.3	1954	7	US-11-292-951-19	Sequence 19, Appl
	40	16.2	70.4	309	7	US-11-266-748A-95119	Sequence 95119, A
c	41	16.2	70.4	309	7	US-11-266-748A-147930	Sequence 147930,
c	42	16.2	70.4	647	7	US-11-266-748A-416821	Sequence 416821,
	43	16.2	70.4	1000	7	US-11-266-748A-198331	Sequence 198331,
c	44	16.2	70.4	1209	6	US-10-449-902-1300	Sequence 1300, Ap
c	45	16.2	70.4	1216	6	US-10-449-902-3674	Sequence 3674, Ap

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-31.rni.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 5.90323 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgatttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20.8	77.0	966	3	US-09-134-001C-53
2	20.2	74.8	1206	3	US-09-248-796A-1184
3	20.2	74.8	14602	2	US-08-597-236-1
4	20.2	74.8	14602	2	US-08-746-682A-1
5	19.8	73.3	1830121	3	US-09-557-884-1
6	19.8	73.3	1830121	3	US-09-643-990A-1

	7	19.8	73.3	1830121	3	US-10-158-865-1	Sequence 1, Appli
	8	19.6	72.6	501	3	US-09-248-796A-4330	Sequence 4330, Ap
c	9	19.6	72.6	3034	5	US-09-430-590E-102	Sequence 102, App
	10	19.6	72.6	44870	3	US-09-949-016-12554	Sequence 12554, A
	11	19.6	72.6	44881	3	US-09-949-016-16349	Sequence 16349, A
	12	19.2	71.1	372	3	US-09-248-796A-1381	Sequence 1381, Ap
c	13	19.2	71.1	2760	3	US-09-198-484-1	Sequence 1, Appli
	14	19.2	71.1	84870	3	US-09-949-016-17547	Sequence 17547, A
c	15	19	70.4	969	3	US-09-830-230A-424	Sequence 424, App
c	16	19	70.4	1020	3	US-09-830-230A-423	Sequence 423, App
c	17	19	70.4	1106	2	US-08-020-245A-2	Sequence 2, Appli
c	18	19	70.4	1106	2	US-08-396-957A-2	Sequence 2, Appli
c	19	19	70.4	2304	2	US-08-020-245A-1	Sequence 1, Appli
c	20	19	70.4	2304	2	US-08-396-957A-1	Sequence 1, Appli
	21	18.8	69.6	6507	3	US-09-949-016-15053	Sequence 15053, A
c	22	18.8	69.6	48691	3	US-09-949-016-16308	Sequence 16308, A
	23	18.6	68.9	650	3	US-09-669-751-180	Sequence 180, App
	24	18.6	68.9	816	3	US-09-270-767-13129	Sequence 13129, A
	25	18.6	68.9	44100	3	US-09-719-554-63	Sequence 63, Appl
	26	18.6	68.9	45484	3	US-09-949-016-12967	Sequence 12967, A
	27	18.6	68.9	50000	3	US-09-662-254B-23	Sequence 23, Appl
	28	18.6	68.9	132871	3	US-09-949-016-13863	Sequence 13863, A
	29	18.6	68.9	161607	3	US-09-949-016-12210	Sequence 12210, A
c	30	18.6	68.9	818128	3	US-09-949-016-14546	Sequence 14546, A
c	31	18.6	68.9	818128	3	US-09-949-016-14547	Sequence 14547, A
c	32	18.6	68.9	818128	3	US-09-949-016-14548	Sequence 14548, A
c	33	18.6	68.9	818128	3	US-09-949-016-14549	Sequence 14549, A
c	34	18.6	68.9	818128	3	US-09-949-016-14550	Sequence 14550, A
c	35	18.6	68.9	818128	3	US-09-949-016-14551	Sequence 14551, A
c	36	18.6	68.9	818128	3	US-09-949-016-14552	Sequence 14552, A
c	37	18.6	68.9	818128	3	US-09-949-016-14553	Sequence 14553, A
c	38	18.6	68.9	818128	3	US-09-949-016-14554	Sequence 14554, A
c	39	18.6	68.9	818128	3	US-09-949-016-14555	Sequence 14555, A
c	40	18.6	68.9	818128	3	US-09-949-016-14556	Sequence 14556, A
c	41	18.6	68.9	818128	3	US-09-949-016-14557	Sequence 14557, A
c	42	18.6	68.9	818128	3	US-09-949-016-14558	Sequence 14558, A
c	43	18.6	68.9	818128	3	US-09-949-016-14559	Sequence 14559, A
c	44	18.6	68.9	818128	3	US-09-949-016-14560	Sequence 14560, A
c	45	18.6	68.9	818128	3	US-09-949-016-14561	Sequence 14561, A

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-31.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 3.93548 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgatttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	19.8	73.3	138443	7	US-11-266-748A-60103	Sequence 60103, A
c 2	19.6	72.6	480	7	US-11-266-748A-14601	Sequence 14601, A
c 3	19.6	72.6	1000	7	US-11-266-748A-283079	Sequence 283079,
4	19.6	72.6	1000	7	US-11-266-748A-309719	Sequence 309719,
c 5	19.6	72.6	3034	7	US-11-238-031-102	Sequence 102, App
c 6	19.6	72.6	4860	7	US-11-266-748A-29410	Sequence 29410, A
7	19	70.4	663	7	US-11-199-489A-21	Sequence 21, Appl
8	19	70.4	1000	7	US-11-266-748A-204243	Sequence 204243,

	9	18.8	69.6	684973	7	US-11-266-748A-32013	Sequence 32013, A
c	10	18.6	68.9	265	7	US-11-266-748A-369240	Sequence 369240,
	11	18.6	68.9	265	7	US-11-266-748A-452619	Sequence 452619,
c	12	18.6	68.9	344	7	US-11-266-748A-5696	Sequence 5696, Ap
c	13	18.6	68.9	608	7	US-11-266-748A-81406	Sequence 81406, A
	14	18.6	68.9	608	7	US-11-266-748A-134217	Sequence 134217,
c	15	18.6	68.9	958	7	US-11-266-748A-57125	Sequence 57125, A
c	16	18.6	68.9	958	7	US-11-266-748A-224637	Sequence 224637,
	17	18.6	68.9	1000	7	US-11-266-748A-200345	Sequence 200345,
	18	18.6	68.9	1000	7	US-11-266-748A-206315	Sequence 206315,
c	19	18.6	68.9	1091	7	US-11-266-748A-256695	Sequence 256695,
	20	18.6	68.9	1091	7	US-11-266-748A-317212	Sequence 317212,
	21	18.6	68.9	1337	6	US-10-953-349-22500	Sequence 22500, A
	22	18.6	68.9	1430	7	US-11-216-545-7445	Sequence 7445, Ap
c	23	18.6	68.9	1703	7	US-11-266-748A-357507	Sequence 357507,
c	24	18.6	68.9	1703	7	US-11-266-748A-386400	Sequence 386400,
	25	18.6	68.9	1703	7	US-11-266-748A-440886	Sequence 440886,
	26	18.6	68.9	56093	7	US-11-266-748A-61305	Sequence 61305, A
c	27	18.6	68.9	340000	7	US-11-266-748A-61353	Sequence 61353, A
	28	18.6	68.9	1071650	7	US-11-266-748A-22664	Sequence 22664, A
c	29	18.2	67.4	311	7	US-11-266-748A-166009	Sequence 166009,
	30	18.2	67.4	311	7	US-11-266-748A-244142	Sequence 244142,
	31	18.2	67.4	885	7	US-11-266-748A-118748	Sequence 118748,
c	32	18.2	67.4	885	7	US-11-266-748A-160912	Sequence 160912,
	33	18.2	67.4	1051	7	US-11-266-748A-85113	Sequence 85113, A
c	34	18.2	67.4	1051	7	US-11-266-748A-137924	Sequence 137924,
	35	18.2	67.4	1656	7	US-11-217-529-78831	Sequence 78831, A
c	36	18.2	67.4	3132	7	US-11-217-529-77436	Sequence 77436, A
c	37	18.2	67.4	3357	6	US-10-449-902-21840	Sequence 21840, A
	38	18.2	67.4	5040	6	US-10-449-902-24467	Sequence 24467, A
c	39	18.2	67.4	684973	7	US-11-266-748A-32013	Sequence 32013, A
c	40	18	66.7	511	7	US-11-266-748A-17986	Sequence 17986, A
c	41	18	66.7	983	7	US-11-266-748A-267502	Sequence 267502,
	42	18	66.7	983	7	US-11-266-748A-328019	Sequence 328019,
	43	18	66.7	1000	7	US-11-266-748A-212714	Sequence 212714,
	44	18	66.7	1318	7	US-11-266-748A-58178	Sequence 58178, A
	45	18	66.7	1508	6	US-10-449-902-4960	Sequence 4960, Ap

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-31.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:48:31 ; Search time 44.4624 Seconds
(without alignments)
7461.730 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgattttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	21.8	80.7	582	4	US-09-925-065A-346391	Sequence 346391,
2	21.8	80.7	582	5	US-09-925-065A-346391	Sequence 346391,
3	21.8	80.7	632	12	US-10-301-480-209648	Sequence 209648,
4	21.8	80.7	632	12	US-10-301-480-823057	Sequence 823057,
5	21.8	80.7	634	4	US-09-925-065A-110091	Sequence 110091,
6	21.8	80.7	634	5	US-09-925-065A-110091	Sequence 110091,
7	21.8	80.7	634	12	US-10-301-480-214207	Sequence 214207,
8	21.8	80.7	634	12	US-10-301-480-827616	Sequence 827616,
c 9	21.8	80.7	638	4	US-09-925-065A-115221	Sequence 115221,
c 10	21.8	80.7	638	5	US-09-925-065A-115221	Sequence 115221,
11	20.8	77.0	966	8	US-10-724-972A-2913	Sequence 2913, Ap
c 12	20.2	74.8	536	8	US-10-424-599-128789	Sequence 128789,
c 13	20.2	74.8	600	6	US-10-027-632-226907	Sequence 226907,
c 14	20.2	74.8	600	7	US-10-027-632-226907	Sequence 226907,
c 15	19.8	73.3	544	12	US-10-301-480-518239	Sequence 518239,
c 16	19.8	73.3	544	12	US-10-301-480-1131648	Sequence 1131648,
c 17	19.8	73.3	547	4	US-09-925-065A-461262	Sequence 461262,
c 18	19.8	73.3	547	5	US-09-925-065A-461262	Sequence 461262,
c 19	19.8	73.3	600	16	US-11-052-554A-468	Sequence 468, App
c 20	19.8	73.3	729	12	US-10-301-480-536352	Sequence 536352,
c 21	19.8	73.3	729	12	US-10-301-480-1149761	Sequence 1149761,
c 22	19.8	73.3	902	12	US-10-301-480-536351	Sequence 536351,
c 23	19.8	73.3	902	12	US-10-301-480-1149760	Sequence 1149760,
24	19.8	73.3	1765	10	US-10-795-159-281	Sequence 281, App
25	19.8	73.3	302250	3	US-09-962-832-154	Sequence 154, App
c 26	19.8	73.3	302250	3	US-09-962-832-154	Sequence 154, App
27	19.8	73.3	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
c 28	19.8	73.3	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
29	19.8	73.3	417576	10	US-10-795-159-684	Sequence 684, App
30	19.8	73.3	1830121	8	US-10-329-670-1	Sequence 1, Appli
31	19.8	73.3	1830121	9	US-10-158-865-1	Sequence 1, Appli
32	19.8	73.3	1830121	10	US-10-981-687-1	Sequence 1, Appli
c 33	19.6	72.6	347	3	US-09-732-627A-3962	Sequence 3962, Ap
34	19.6	72.6	444	4	US-09-925-065A-599994	Sequence 599994,
35	19.6	72.6	444	5	US-09-925-065A-599994	Sequence 599994,
36	19.6	72.6	444	12	US-10-301-480-22564	Sequence 22564, A
37	19.6	72.6	444	12	US-10-301-480-635973	Sequence 635973,
38	19.6	72.6	472	6	US-10-027-632-96609	Sequence 96609, A
39	19.6	72.6	472	6	US-10-027-632-319014	Sequence 319014,
40	19.6	72.6	472	7	US-10-027-632-96609	Sequence 96609, A
41	19.6	72.6	472	7	US-10-027-632-319014	Sequence 319014,
c 42	19.6	72.6	551	3	US-09-867-701-6279	Sequence 6279, Ap
43	19.6	72.6	819	8	US-10-282-122A-34171	Sequence 34171, A
c 44	19.6	72.6	1923	10	US-10-750-185-38883	Sequence 38883, A
c 45	19.6	72.6	1923	10	US-10-750-623-38883	Sequence 38883, A

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-10.ra1.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:22:56 ; Search time 31 Seconds
(without alignments)
2272.973 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4271	98.8	894	1	US-08-599-455B-2	Sequence 2, Appli
2	4271	98.8	894	2	US-09-069-781B-2	Sequence 2, Appli
3	4271	98.8	894	2	US-08-618-957A-12	Sequence 12, Appl
4	4271	98.8	894	2	US-09-137-132-2	Sequence 2, Appli
5	4271	98.8	894	2	US-08-864-564A-2	Sequence 2, Appli
6	4271	98.8	894	2	US-09-094-410-2	Sequence 2, Appli
7	4271	98.8	894	2	US-08-708-123D-2	Sequence 2, Appli
8	4271	98.8	894	2	US-08-583-153A-2	Sequence 2, Appli
9	4271	98.8	894	2	US-08-570-142D-2	Sequence 2, Appli

10	4271	98.8	894	2	US-08-638-524B-2	Sequence 2, Appli
11	4271	98.8	894	2	US-10-095-929-12	Sequence 12, Appl
12	4271	98.8	894	2	US-09-950-149-2	Sequence 2, Appli
13	4271	98.8	1162	1	US-08-599-455B-43	Sequence 43, Appl
14	4271	98.8	1162	2	US-09-069-781B-43	Sequence 43, Appl
15	4271	98.8	1162	2	US-09-137-132-43	Sequence 43, Appl
16	4271	98.8	1162	2	US-08-864-564A-43	Sequence 43, Appl
17	4271	98.8	1162	2	US-09-094-410-43	Sequence 43, Appl
18	4271	98.8	1162	2	US-08-708-123D-43	Sequence 43, Appl
19	4271	98.8	1162	2	US-08-638-524B-43	Sequence 43, Appl
20	4271	98.8	1162	2	US-09-950-149-43	Sequence 43, Appl
21	4147	96.0	896	1	US-08-640-389A-12	Sequence 12, Appl
22	4031	93.3	783	2	US-08-780-562-7	Sequence 7, Appli
23	3991	92.4	1162	2	US-08-803-346-1	Sequence 1, Appli
24	3983	92.2	895	2	US-08-827-962-19	Sequence 19, Appl
25	3983	92.2	1162	2	US-08-827-962-15	Sequence 15, Appl
26	3977	92.0	1162	2	US-08-827-962-20	Sequence 20, Appl
27	3947	91.3	895	2	US-08-827-962-21	Sequence 21, Appl
28	3355	77.6	804	2	US-09-116-676-10	Sequence 10, Appl
29	3340	77.3	896	2	US-08-780-562-3	Sequence 3, Appli
30	3340	77.3	923	2	US-08-780-562-4	Sequence 4, Appli
31	3340	77.3	1165	1	US-08-599-455B-4	Sequence 4, Appli
32	3340	77.3	1165	2	US-09-093-814-1	Sequence 1, Appli
33	3340	77.3	1165	2	US-09-069-781B-4	Sequence 4, Appli
34	3340	77.3	1165	2	US-08-618-957A-11	Sequence 11, Appl
35	3340	77.3	1165	2	US-09-137-132-4	Sequence 4, Appli
36	3340	77.3	1165	2	US-09-094-410-4	Sequence 4, Appli
37	3340	77.3	1165	2	US-08-708-123D-4	Sequence 4, Appli
38	3340	77.3	1165	2	US-08-583-153A-4	Sequence 4, Appli
39	3340	77.3	1165	2	US-08-570-142D-4	Sequence 4, Appli
40	3340	77.3	1165	2	US-08-780-562-2	Sequence 2, Appli
41	3340	77.3	1165	2	US-08-638-524B-4	Sequence 4, Appli
42	3340	77.3	1165	2	US-10-095-929-11	Sequence 11, Appl
43	3340	77.3	1165	2	US-09-950-149-4	Sequence 4, Appli
44	3328	77.0	896	2	US-08-618-957A-10	Sequence 10, Appl
45	3328	77.0	896	2	US-09-357-914-33	Sequence 33, Appl

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-10.rapbm.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:23:16 ; Search time 91 Seconds
(without alignments)
4097.670 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKIFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB ID	Description
		Match				
1	4271	98.8	894	2	US-08-779-457-51	Sequence 51, Appl
2	4271	98.8	894	4	US-10-079-625-2	Sequence 2, Appli
3	4271	98.8	894	4	US-10-095-929-12	Sequence 12, Appl
4	4271	98.8	894	5	US-10-921-710-51	Sequence 51, Appl
5	4271	98.8	894	6	US-11-026-133-12	Sequence 12, Appl
6	4271	98.8	894	6	US-11-202-330-2	Sequence 2, Appli
7	4271	98.8	1162	4	US-10-079-625-43	Sequence 43, Appl
8	4271	98.8	1162	6	US-11-202-330-43	Sequence 43, Appl
9	4265	98.7	1162	4	US-10-226-579-2	Sequence 2, Appli
10	4031	93.3	783	2	US-08-779-457-7	Sequence 7, Appli

11	4031	93.3	783	4	US-10-214-802-7	Sequence 7, Appli
12	4031	93.3	783	5	US-10-921-710-7	Sequence 7, Appli
13	4031	93.3	783	6	US-11-192-219-7	Sequence 7, Appli
14	3355	77.6	804	3	US-09-116-676-10	Sequence 10, Appl
15	3340	77.3	896	2	US-08-779-457-3	Sequence 3, Appli
16	3340	77.3	896	4	US-10-214-802-3	Sequence 3, Appli
17	3340	77.3	896	4	US-10-373-624A-2	Sequence 2, Appli
18	3340	77.3	896	5	US-10-774-721-10	Sequence 10, Appl
19	3340	77.3	896	5	US-10-921-710-3	Sequence 3, Appli
20	3340	77.3	896	6	US-11-192-219-3	Sequence 3, Appli
21	3340	77.3	923	2	US-08-779-457-4	Sequence 4, Appli
22	3340	77.3	923	4	US-10-214-802-4	Sequence 4, Appli
23	3340	77.3	923	5	US-10-921-710-4	Sequence 4, Appli
24	3340	77.3	923	6	US-11-192-219-4	Sequence 4, Appli
25	3340	77.3	925	5	US-10-492-403A-15	Sequence 15, Appl
26	3340	77.3	1165	2	US-08-779-457-2	Sequence 2, Appli
27	3340	77.3	1165	3	US-09-894-039-1	Sequence 1, Appli
28	3340	77.3	1165	4	US-10-095-929-11	Sequence 11, Appl
29	3340	77.3	1165	4	US-10-214-802-2	Sequence 2, Appli
30	3340	77.3	1165	4	US-10-226-579-4	Sequence 4, Appli
31	3340	77.3	1165	5	US-10-921-710-2	Sequence 2, Appli
32	3340	77.3	1165	5	US-10-893-315-73	Sequence 73, Appl
33	3340	77.3	1165	6	US-11-026-133-11	Sequence 11, Appl
34	3340	77.3	1165	6	US-11-192-219-2	Sequence 2, Appli
35	3340	77.3	1165	6	US-11-202-330-4	Sequence 4, Appli
36	3333	77.1	1167	5	US-10-893-315-87	Sequence 87, Appl
37	3328	77.0	896	4	US-10-095-929-10	Sequence 10, Appl
38	3328	77.0	896	6	US-11-026-133-10	Sequence 10, Appl
39	3328	77.0	906	4	US-10-095-929-9	Sequence 9, Appli
40	3328	77.0	906	6	US-11-026-133-9	Sequence 9, Appli
41	3328	77.0	958	4	US-10-095-929-8	Sequence 8, Appli
42	3328	77.0	958	6	US-11-026-133-8	Sequence 8, Appli
43	3326	77.0	1165	4	US-10-079-625-4	Sequence 4, Appli
44	3323	76.9	960	4	US-10-095-929-3	Sequence 3, Appli
45	3323	76.9	960	6	US-11-026-133-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:23:56 ; Search time 12 Seconds
(without alignments)
1584.487 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	250.5	5.8	836	6	US-10-511-937-2988	Sequence 2988, Ap
2	194.5	4.5	422	7	US-11-296-092-32	Sequence 32, Appl
3	194.5	4.5	422	7	US-11-296-155-32	Sequence 32, Appl
4	154	3.6	368	6	US-10-449-902-38075	Sequence 38075, A
5	151	3.5	1180	6	US-10-505-928-459	Sequence 459, App
6	149	3.4	229	7	US-11-297-134-8	Sequence 8, Appli
7	149	3.4	2355	7	US-11-105-233-158	Sequence 158, App
8	136.5	3.2	635	6	US-10-511-937-2424	Sequence 2424, Ap

9	136	3.1	428	7	US-11-274-375-8	Sequence 8, Appli
10	136	3.1	629	7	US-11-274-375-10	Sequence 10, Appl
11	133.5	3.1	1998	7	US-11-348-606-3	Sequence 3, Appli
12	127	2.9	903	7	US-11-293-697-2977	Sequence 2977, Ap
13	126.5	2.9	1037	7	US-11-259-133-12	Sequence 12, Appl
14	126	2.9	337	7	US-11-274-375-2	Sequence 2, Appli
15	126	2.9	428	7	US-11-274-375-4	Sequence 4, Appli
16	126	2.9	629	7	US-11-274-375-6	Sequence 6, Appli
17	117.5	2.7	1015	7	US-11-259-133-14	Sequence 14, Appl
18	113.5	2.6	1279	6	US-10-449-902-53619	Sequence 53619, A
19	111.5	2.6	972	7	US-11-255-147-8	Sequence 8, Appli
20	111.5	2.6	972	7	US-11-248-956-5	Sequence 5, Appli
21	110.5	2.6	991	7	US-11-165-586-62	Sequence 62, Appl
22	108	2.5	650	6	US-10-509-131-11	Sequence 11, Appl
23	105	2.4	825	6	US-10-505-928-650	Sequence 650, App
24	105	2.4	825	6	US-10-511-937-3001	Sequence 3001, Ap
25	103	2.4	984	7	US-11-259-133-22	Sequence 22, Appl
26	103	2.4	1042	7	US-11-121-154-176	Sequence 176, App
27	102.5	2.4	306	6	US-10-471-571A-700	Sequence 700, App
28	102	2.4	1215	6	US-10-505-928-75	Sequence 75, Appl
29	101.5	2.3	539	7	US-11-259-133-8	Sequence 8, Appli
30	101.5	2.3	983	7	US-11-302-678-2	Sequence 2, Appli
31	101.5	2.3	983	7	US-11-259-133-6	Sequence 6, Appli
32	101.5	2.3	1650	7	US-11-175-714-70	Sequence 70, Appl
33	100.5	2.3	1134	6	US-10-449-902-51943	Sequence 51943, A
34	100	2.3	1005	7	US-11-259-133-20	Sequence 20, Appl
35	99	2.3	720	6	US-10-196-749-170	Sequence 170, App
36	99	2.3	720	7	US-11-101-316-38	Sequence 38, Appl
37	98.5	2.3	380	7	US-11-220-888-4	Sequence 4, Appli
38	98.5	2.3	380	7	US-11-331-993-2	Sequence 2, Appli
39	98.5	2.3	1204	7	US-11-289-102-236	Sequence 236, App
40	98	2.3	600	7	US-11-293-697-4457	Sequence 4457, Ap
41	97.5	2.3	310	7	US-11-220-888-1	Sequence 1, Appli
42	97.5	2.3	984	7	US-11-283-329-104	Sequence 104, App
43	97.5	2.3	1871	6	US-10-501-834-26	Sequence 26, Appl
44	97	2.2	439	7	US-11-297-134-22	Sequence 22, Appl
45	97	2.2	5635	6	US-10-766-760-2	Sequence 2, Appli

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-9.rni.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 538.068 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-9
Perfect score: 2461
Sequence: 1 gaggaatcggttctgcaaatc.....ctgtacttttcatggattag 2461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2433.4	98.9	3097	2 US-08-599-455B-1	Sequence 1, Appli
2	2433.4	98.9	3097	3 US-09-069-781B-1	Sequence 1, Appli
3	2433.4	98.9	3097	3 US-09-137-132-1	Sequence 1, Appli
4	2433.4	98.9	3097	3 US-08-864-564A-1	Sequence 1, Appli
5	2433.4	98.9	3097	3 US-09-094-410-1	Sequence 1, Appli
6	2433.4	98.9	3097	3 US-08-708-123D-1	Sequence 1, Appli

7	2433.4	98.9	3097	3	US-08-583-153A-1	Sequence 1, Appli
8	2433.4	98.9	3097	3	US-08-570-142D-1	Sequence 1, Appli
9	2433.4	98.9	3097	3	US-08-638-524B-1	Sequence 1, Appli
10	2433.4	98.9	3097	4	US-09-950-149-1	Sequence 1, Appli
11	2433.4	98.9	3854	2	US-08-599-455B-42	Sequence 42, Appl
12	2433.4	98.9	3854	3	US-09-069-781B-42	Sequence 42, Appl
13	2433.4	98.9	3854	3	US-09-137-132-42	Sequence 42, Appl
14	2433.4	98.9	3854	3	US-08-864-564A-42	Sequence 42, Appl
15	2433.4	98.9	3854	3	US-09-094-410-42	Sequence 42, Appl
16	2433.4	98.9	3854	3	US-08-708-123D-42	Sequence 42, Appl
17	2433.4	98.9	3854	3	US-08-638-524B-42	Sequence 42, Appl
18	2433.4	98.9	3854	4	US-09-950-149-42	Sequence 42, Appl
19	2364.6	96.1	2868	3	US-08-780-562-8	Sequence 8, Appli
20	2163.4	87.9	3495	3	US-08-827-962-17	Sequence 17, Appl
21	2163.4	87.9	3650	3	US-08-837-635-5	Sequence 5, Appli
22	2163.4	87.9	3650	3	US-08-803-346-2	Sequence 2, Appli
23	2161.8	87.8	3650	3	US-08-837-635-7	Sequence 7, Appli
24	2160.2	87.8	3650	3	US-08-827-962-16	Sequence 16, Appl
25	1692.2	68.8	3102	3	US-08-780-562-6	Sequence 6, Appli
26	1692.2	68.8	3629	3	US-08-837-635-6	Sequence 6, Appli
27	1692.2	68.8	3800	3	US-09-023-655-885	Sequence 885, App
28	1692.2	68.8	3871	2	US-08-599-455B-3	Sequence 3, Appli
29	1692.2	68.8	3871	3	US-09-069-781B-3	Sequence 3, Appli
30	1692.2	68.8	3871	3	US-09-137-132-3	Sequence 3, Appli
31	1692.2	68.8	3871	3	US-09-094-410-3	Sequence 3, Appli
32	1692.2	68.8	3871	3	US-08-708-123D-3	Sequence 3, Appli
33	1692.2	68.8	3871	3	US-08-583-153A-3	Sequence 3, Appli
34	1692.2	68.8	3871	3	US-08-570-142D-3	Sequence 3, Appli
35	1692.2	68.8	3871	3	US-08-638-524B-3	Sequence 3, Appli
36	1692.2	68.8	3871	4	US-09-950-149-3	Sequence 3, Appli
37	1692.2	68.8	4102	3	US-08-780-562-1	Sequence 1, Appli
38	1691	68.7	3004	3	US-08-780-562-5	Sequence 5, Appli
39	1690.8	68.7	2877	2	US-08-693-697-35	Sequence 35, Appl
40	1690.8	68.7	2880	2	US-08-693-697-32	Sequence 32, Appl
41	1690.8	68.7	2991	2	US-08-355-888A-6	Sequence 6, Appli
42	1690.8	68.7	2991	2	US-08-588-190-1	Sequence 1, Appli
43	1690.8	68.7	2991	2	US-08-693-697-6	Sequence 6, Appli
44	1690.8	68.7	2991	2	US-08-640-389A-1	Sequence 1, Appli
45	1690.8	68.7	2991	3	US-08-693-696-6	Sequence 6, Appli

SCORE Search Results Details for Application 08783734 and Search Result us-08-783-734d-9.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-9.rnpbm.

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OM nucleic - nucleic search, using sw model

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Run on:      June 29, 2006, 19:48:31 ; Search time 4052.66 Seconds
              (without alignments)
              7461.730 Million cell updates/sec
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2433.4	98.9	3097	6	US-10-079-625-1	Sequence 1, Appli
2	2433.4	98.9	3097	16	US-11-202-330-1	Sequence 1, Appli
3	2433.4	98.9	3656	6	US-10-226-579-1	Sequence 1, Appli
4	2433.4	98.9	3854	6	US-10-079-625-42	Sequence 42, Appl
5	2433.4	98.9	3854	16	US-11-202-330-42	Sequence 42, Appl
6	2390.4	97.1	2679	6	US-10-278-733-14	Sequence 14, Appl
7	2364.6	96.1	2868	2	US-08-779-457-8	Sequence 8, Appli
8	2364.6	96.1	2868	6	US-10-214-802-8	Sequence 8, Appli
9	2364.6	96.1	2868	9	US-10-921-710-8	Sequence 8, Appli
10	2364.6	96.1	2868	15	US-11-192-219-8	Sequence 8, Appli
11	2165.6	88.0	3799	16	US-11-136-527-2058	Sequence 2058, Ap
12	2148.8	87.3	3489	6	US-10-278-733-18	Sequence 18, Appl
13	1692.2	68.8	3102	2	US-08-779-457-6	Sequence 6, Appli
14	1692.2	68.8	3102	6	US-10-214-802-6	Sequence 6, Appli
15	1692.2	68.8	3102	9	US-10-921-710-6	Sequence 6, Appli
16	1692.2	68.8	3102	15	US-11-192-219-6	Sequence 6, Appli
17	1692.2	68.8	3800	6	US-10-226-579-3	Sequence 3, Appli
18	1692.2	68.8	3800	8	US-10-641-643-885	Sequence 885, App
19	1692.2	68.8	3800	10	US-10-893-315-12	Sequence 12, Appl
20	1692.2	68.8	3871	16	US-11-202-330-3	Sequence 3, Appli
21	1692.2	68.8	4102	2	US-08-779-457-1	Sequence 1, Appli
22	1692.2	68.8	4102	6	US-10-214-802-1	Sequence 1, Appli
23	1692.2	68.8	4102	9	US-10-921-710-1	Sequence 1, Appli
24	1692.2	68.8	4102	15	US-11-192-219-1	Sequence 1, Appli
25	1691	68.7	3004	2	US-08-779-457-5	Sequence 5, Appli
26	1691	68.7	3004	6	US-10-214-802-5	Sequence 5, Appli
27	1691	68.7	3004	9	US-10-921-710-5	Sequence 5, Appli
28	1691	68.7	3004	15	US-11-192-219-5	Sequence 5, Appli
29	1690.8	68.7	2991	6	US-10-095-929-1	Sequence 1, Appli
30	1690.8	68.7	2991	13	US-11-026-133-1	Sequence 1, Appli
31	1689	68.6	3784	10	US-10-893-315-26	Sequence 26, Appl
32	1688.2	68.6	2415	3	US-09-116-676-9	Sequence 9, Appli
33	1687.4	68.6	3871	6	US-10-079-625-3	Sequence 3, Appli
34	1682.8	68.4	2877	6	US-10-245-616-1	Sequence 1, Appli
35	1682.8	68.4	2877	15	US-11-166-730-1	Sequence 1, Appli
36	1680.4	68.3	3909	9	US-10-014-156-12	Sequence 12, Appl
37	1676	68.1	2691	8	US-10-373-624A-1	Sequence 1, Appli
38	1676	68.1	2691	9	US-10-774-721-9	Sequence 9, Appli
39	1613.8	65.6	2751	8	US-10-373-624A-3	Sequence 3, Appli
40	1613.8	65.6	3486	8	US-10-373-624A-7	Sequence 7, Appli
41	1613.8	65.6	3486	9	US-10-774-721-13	Sequence 13, Appl
42	1613.8	65.6	3705	8	US-10-373-624A-5	Sequence 5, Appli
43	1613.8	65.6	3705	9	US-10-774-721-11	Sequence 11, Appl
44	1540	62.6	5147	6	US-10-116-802-93	Sequence 93, Appl
45	480.4	19.5	630	10	US-10-803-459C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-9.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 358.712 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-9
Perfect score: 2461
Sequence: 1 gaggaatcgttctgcaaatc.....ctgtacttttcatggattag 2461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
	1	1692.2	68.8	5157	7	US-11-266-748A-56701
	2	1676	68.1	4968	7	US-11-266-748A-31964
	3	1087.8	44.2	1538	7	US-11-266-748A-250506
c	4	1087.8	44.2	1538	7	US-11-266-748A-311023
	5	554.2	22.5	756	7	US-11-266-748A-368606
c	6	554.2	22.5	756	7	US-11-266-748A-451985
	7	338.8	13.8	1000	7	US-11-266-748A-220684
	8	338.8	13.8	1000	7	US-11-266-748A-284131

c	9	338.8	13.8	1000	7	US-11-266-748A-335560	Sequence 335560,
	10	338.8	13.8	1000	7	US-11-266-748A-394020	Sequence 394020,
c	11	338.8	13.8	1000	7	US-11-266-748A-465066	Sequence 465066,
	12	179.4	7.3	540	7	US-11-266-748A-52634	Sequence 52634, A
	13	179.4	7.3	965	7	US-11-266-748A-250812	Sequence 250812,
c	14	179.4	7.3	965	7	US-11-266-748A-311329	Sequence 311329,
	15	116	4.7	659	7	US-11-266-748A-47098	Sequence 47098, A
	16	39	1.6	3085	7	US-11-266-748A-28955	Sequence 28955, A
	17	35.8	1.5	291	7	US-11-266-748A-8149	Sequence 8149, Ap
	18	35.6	1.4	726	6	US-10-471-571A-5187	Sequence 5187, Ap
c	19	35.2	1.4	639	7	US-11-266-748A-52821	Sequence 52821, A
c	20	35.2	1.4	722	7	US-11-266-748A-79651	Sequence 79651, A
c	21	35.2	1.4	722	7	US-11-266-748A-110622	Sequence 110622,
	22	35.2	1.4	722	7	US-11-266-748A-132462	Sequence 132462,
c	23	35.2	1.4	816	7	US-11-266-748A-163458	Sequence 163458,
c	24	35.2	1.4	907	7	US-11-266-748A-79652	Sequence 79652, A
c	25	35.2	1.4	907	7	US-11-266-748A-110623	Sequence 110623,
	26	35.2	1.4	907	7	US-11-266-748A-132463	Sequence 132463,
c	27	35.2	1.4	1527	7	US-11-266-748A-348151	Sequence 348151,
c	28	35.2	1.4	1527	7	US-11-266-748A-381638	Sequence 381638,
	29	35.2	1.4	1527	7	US-11-266-748A-431530	Sequence 431530,
c	30	35.2	1.4	1834	7	US-11-266-748A-185027	Sequence 185027,
c	31	35.2	1.4	1834	7	US-11-266-748A-192533	Sequence 192533,
	32	34.8	1.4	1474	7	US-11-266-748A-27239	Sequence 27239, A
	33	34.4	1.4	3033	7	US-11-293-697-103	Sequence 103, App
c	34	34.2	1.4	1804	6	US-10-953-349-11271	Sequence 11271, A
c	35	34	1.4	599	6	US-10-449-902-4612	Sequence 4612, Ap
	36	34	1.4	1062	6	US-10-449-902-2289	Sequence 2289, Ap
	37	34	1.4	3642	7	US-11-217-529-79570	Sequence 79570, A
	38	34	1.4	4192	7	US-11-266-748A-56124	Sequence 56124, A
c	39	33.8	1.4	1058	7	US-11-266-748A-166553	Sequence 166553,
	40	33.8	1.4	3152	7	US-11-266-748A-348490	Sequence 348490,
	41	33.8	1.4	3152	7	US-11-266-748A-381851	Sequence 381851,
c	42	33.8	1.4	3152	7	US-11-266-748A-431869	Sequence 431869,
	43	33.8	1.4	150024	7	US-11-266-748A-60141	Sequence 60141, A
	44	33.6	1.4	640	7	US-11-266-748A-41507	Sequence 41507, A
	45	33.6	1.4	992	7	US-11-266-748A-364302	Sequence 364302,